10/536935

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SEQUENCE LISTING

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<120> METHOD OF SCREENING FOR COMPOUNDS THAT INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

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	tt gta ttg gga le Val Leu Gly 245				
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330

1008

1056

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Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser

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_	-			-			tat Tyr 360	_	_	_					
_		-				_	aac Asn				_				
_	-	_	_				tac Tyr	_	_		-	-	-		
_	_				-		gac Asp			-				-	
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1104

1152

1200

1248

1296

1344

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Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser 50 55 60

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420 425 430

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att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240 Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val 65 70 75 80

att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
85 90 95

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	gtt Val		_					-		_	-			_		528
-	atc Ile	-									_		_	_		576
-	aaa Lys			_	_				_						_	624
	gga Gly 210	-		_		_	_	-	_		-	_		_	_	672
	gaa Glu															720
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Ser Ser Tyr 35	20	25			
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35 Ala Leu Ile 50 Ile Thr Val 65	Leu Ser Phe Tyr Asp Tyr Tyr Ser Asn 70	Arg Leu Leu 40 Ile Leu Asn 55 Ser Pro Ser	Lys Lys Service Val Leu The Go	30 r Leu Gly Asp 45 r Ile Leu Ala 0	Leu Ser Val 80

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Gly	Val	Gly	Ser	Phe 165	Val	Phe	Ser	Met	Gly 170	Leu	Ala	Asn	Ser	Arg 175	Gln
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Ile	Phe	Leu 435	Val	Ser	Asn	Leu	Leu 440	Thr	Gly	Phe	Ile	Asn 445	Met	Ser	Ile
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aat ctt ggg ttt Asn Leu Gly Phe 50			_	
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Met i	Asp	Leu	Gly	Val 165	Gly	Ser	Phe	Met	Phe 170	Ser	Ser	Gly	Thr	Val 175	Ala	
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tgg a																624
acg a		_					_		_	-	_			_		672
tgg a Trp 2 225									_	-			_			720
ttt (Phe <i>i</i>																768
att a Ile '						_	_		_							816
tgg (Trp 2										_	_	_		_	-	864
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tat a Tyr ' 305			-	-	_	_	_	_	_			_			_	960
gct (Ala (_	_	Trp	_	Arg		Gln	Arg	Leu	Leu	Phe	_		_		1008
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cgc (Arg)																1104
atg :																1152
tct s Ser s 385						_	_	_			_		_	_	-	1200
aat a Asn a																1248

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Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu 50 55 60

Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile 65 70 75 80

Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn 85 90 95

Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn 100 105 110

Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser 115 120 · 125

Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr 130 140

Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu 145 150 155 160

Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala 165 170 175

Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu 180 185 190

Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu
195 200 205

Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His

210 215 220

Trp Asn Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe 230 235 Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe 245 250 Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met 295 Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg 315 Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile 325 335 Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser 345 Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn 355 360 365 Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro 375 Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala 385 390 395 Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly 405 410 Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly 420 425 430 Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His

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455

440

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<220>

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			_							tac Tyr	_	_	_	_		198
	_	_		_			_			atc Ile	_		_			246
										ctc Leu						294
										cct Pro						342
										ggg Gly 115						390
										att Ile						438
										tgc Cys						486
										gcc Ala						534
										tcg Ser						582
										agc Ser 195						630
										gcg Ala						678
att Ile	cct Pro	ctg Leu	ctc Leu 220	gtc Val	ctc Leu	ggc Gly	ctg Leu	att Ile 225	cgg Arg	cta Leu	tac Tyr	agc Ser	gtc Val 230	aaa Lys	ggc Gly	726
										ggc Gly						774

						ttg Leu 255										822
						tca Ser										870
						cta Leu										918
						cca Pro										966
						tat Tyr										1014
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						gtc Val										1110
						gtg Val										1158
						tcc Ser										1206
						aac Asn										1254
						cct Pro 415										1302
						gat Asp										1350
						gcg Ala										1398
						atc Ile										1446
						gga Gly										1494
cta	gca	ttg	cat	cat	gcc	aat	atc	aaa	gta	ctt	cct	ttc	tag			1536

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1576

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Val Ser Val Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe 35 40 45

Thr Pro Tyr Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val 50 55 60

Leu Ala Ile Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu
65 70 75 80

Leu Asn Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr 85 90 95

Lys Arg Pro Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala 100 105 110

Arg Ala Gly Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser 115 120 125

Leu Pro Ile His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val 130 135 140

Ile Thr Cys Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg 145 150 155 160

Arg Phe Ala Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly
165 170 175

Val Gly Ser Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu 180 185 190

Leu Lys Ser Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg 195 200 205

Leu Ile Ala Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu 210 215 220

Ile Arg Leu Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr 225 230 235 240

Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro 245 250 255 Pro Phe Val Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr 265 Glu Val Leu Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu 280 285 Ser Thr Asp Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu 345 Ile Ser Leu Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu 355 Asn Ser Thr Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr 390 395 Ala Gln Leu Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala 410 Val His Arg Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe 420 425 Ala Thr Ser Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile Phe Leu Leu Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser 450 455 Thr Ile Asp Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr 470 475 Ser Ser Ile Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile Lys Val Leu Pro Phe 500 <210> 11 <211> 1648

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190

185

					aaa Lys		_		_	_				 735
					att Ile									783
					ttg Leu									831
					ttc Phe			_		_		_		 879
	-		_	_	ttg Leu 265	-	_						_	927
					gtc Val									975
					ctc Leu									1023
_		_	_		gtc Val									1071
					atc Ile									1119
					gaa Glu 345									1167
					gtg Val						_			1215
					gga Gly									1263
					ctt Leu									1311
					atc Ile									1359
					agc Ser 425									1407

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gcc aat ctt ctg act gga gct gtg aat ctg agc atc tcc aca att gat 15 Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser Thr Ile Asp 455 460 465	503
gct aat aca gcg cag gcc atc gct gtt ctc att gga tat tca tcc att 15 Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr Ser Ser Ile 470 475 480	551
atc aca ggg gtt gct cta gca ttg cat cat gcc aat atc aaa gta ctt 15 Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile Lys Val Leu 485 490 495	599
cct ttc tag ggtatttacg agcaattggt ggtgtgttga agatatatag 16 Pro Phe 500	648
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tgg agt atc aac gct gtc agc ctg gtc gca ctg gtatgtagct cgttctccga 1 Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu 25 30	156
ggggttctgt catttggaga cgcttattaa ttgggatcgc ag gcg aca tat gct Ala Thr Tyr Ala 35	210
ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn	258

	40	45	50	
	s Val Leu Pro	cta tta ttc ggg o Leu Leu Phe Gly V 60		
		tct ttt ttg tcc a Ser Phe Leu Ser 1 75		_
_		tgc ttc aaa tct c Cys Phe Lys Ser V		-
		gac gaa tca gac t Asp Glu Ser Asp S 110		
		gga tct gca gca g Gly Ser Ala Ala V 125		
	r Gln Val Ala	ttc gct tcg gga t Phe Ala Ser Gly S 140		
		tcg cca agt agt t Ser Pro Ser Ser S 155		
		atg ggc gtt aac a Met Gly Val Asn A		
		gtt ccg tca cat a Val Pro Ser His I 190		
		ttg agg ctc aaa a Leu Arg Leu Lys I 205		-
	p Val Lys Glu	aag gga aga tta d Lys Gly Arg Leu E 220		
		atg act gtt atc t Met Thr Val Ile 0 235		
		tgg cag ggc aag t Trp Gln Gly Lys (
act agt ctg gt Thr Ser Leu 260	aagctttc cttca	agccat ggtccagtgc	tcaccgctct	931
		gtc ggg tca ttc Val Gly Ser Phe 270	=	

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													ccg Pro 305			1077
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													tat Tyr			1173
													acc Thr			1221
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_		-				-				_	_		cag Gln 385	_		1317
													cgg Arg			1365
			-		_	-							ggt Gly			1413
													tta Leu			1461
													aat Asn			. 1509
													att Ile 465			1557
													ggc Gly			1605
								cgt Arg		gtaa	agtg	gac a	atcti	ttggt	a	1655
ata	tgta	acc t	tatad	ctaai	tc co	ctgca	ataaa		Ala A				tat q Tyr V	Val I		1707

Trp Val Ala Ala	tac aat ac Tyr Asn Th 505						1755
acc cac att att of Thr His Ile Ile 5					~		1803
tta gtg cct ccc t Leu Val Pro Pro 1 535							1851
ttt ttg gcg gcc a Phe Leu Ala Ala a 550	_	u Thr Gly				_	1899
aca atg tat gcg of Thr Met Tyr Ala 1565							1947
acc ttg aca atc a Thr Leu Thr Ile S							1995
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	ccc Pro															336
	gaa Glu			-		-		-	-			-	_	-		384
	gta Val 130	-									_	_				432
	tct Ser		-	_					_	_		_	_			480
	tca Ser															528
	tcg Ser															576
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Ser	Lys	Val 195	Arg	Ile	Ser	Pro	Val 200	Pro	Tyr	Leu	Arg	Leu 205	Lys	Lys	Ser	
	gca Ala															672
	210					215					220					
	aca Thr															720
	gcg Ala															768
	ttt Phe															816
	ctc Leu															864

Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro 305 310 315 320

cct acg ccc tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr

ccg tcc ccg ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc

295

290

300

912

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								ggc Gly 345								1056
		_	_	_				gcc Ala				-				1104
			_		-			Gly ggg	-				_	_		1152
_	-							caa Gln			-					1200
						_		aag Lys	_							1248
						_		ggc Gly 425	-				_		_	1296
			-				_	aga Arg			_			-		1344
								ttt Phe								1392
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								gta Val								1488
		_			_		-	tac Tyr 505								1536
								cca Pro								1584
		_						ttg Leu		_	-	_				1632
					_		_	aac Asn	_				_			1680
gtg	agc	atg	aag	aca	atg	tat	gcg	ccg	gcg	tgg	ttg	tca	atg	ggg	gtg	1728

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val 565 570 tta atg ttg tat acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa 1776 Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys 580 585 gga cgg agg atc aag ata tag 1797 Gly Arg Arg Ile Lys Ile 595 <210> 14 <211> 598 <212> PRT <213> Cryptococcus neoformans <400> 14 Met Gly Asp Tyr Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro 10 Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu 35 40 Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile 70 Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp 100 105 Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser 120 Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu 130 135 Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser 150 155 Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg 170 Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp 180 185 Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser 200 Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe 215

Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile

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Pro 305	Ser	Pro	Phe	Thr	Ser 310	Ile	Leu	Ile	Ser	Leu 315	Arg	Lys	Ser	Ile	Pro 320
Ile	Leu	Val	Leu	Gly 325	Phe	Ile	Arg	Leu	Ile 330	Met	Val	Lys	Gly	Ser 335	Asp
Tyr	Pro	Glu	His 340	Val	Thr	Glu	Tyr	Gly 345	Val	His	Trp	Asn	Phe 350	Phe	Phe
Thr	Leu	Ala 355	Leu	Val	Pro	Val	Leu 360	Ala	Val	Gly	Ile	Arg 365	Pro	Leu	Thr
Gln	Trp 370	Leu	Arg	Trp	Ser	Val 375	Leu	Gly	Val	Ile	Ile 380	Ser	Leu	Leu	His
Gln 385	Leu	Trp	Leu	Thr	Tyr 390	Tyr	Leu	Gln	Ser	Ile 395	Val	Phe	Ser	Phe	Gly 400
Arg	Ser	Gly	Ile	Phe 405	Leu	Ala	Asn	Lys	Glu 410	Gly	Phe	Ser	Ser	Leu 415	Pro
Gly	Tyr	Leu	Ser 420	Ile	Phe	Leu	Ile	Gly 425	Leu	Ser	Ile	Gly	Asp 430	His	Val
Leu	Arg	Leu 435	Ser	Leu	Pro	Pro	Arg 440	Arg	Glu	Arg	Val	Val 445	Ser	Glu	Thr
Asn	Glu 450	Glu	His	Glu	Gln	Ser 455	His	Phe	Glu	Arg	Lys 460	Lys	Leu	Asp	Leu
Ile 465	Met	Glu	Leu	Ile	Gly 470	Tyr	Ser	Leu	Gly	Trp 475	Trp	Ala	Leu	Leu	Gly 480
Gly	Trp	Ile	Trp	Ala 485	Gly	Gly	Glu	Val	Ser 490	Arg	Arg	Leu	Ala	Asn 495	Ala
Pro	Tyr	Val	Phe 500	Trp	Val	Ala	Ala	Tyr 505	Asn	Thr	Thr	Phe	Leu 510	Leu	Gly
Tyr	Leu	Leu 515	Leu	Thr	His	Ile	Ile 520	Pro	Ser	Pro	Thr	Ser 525	Ser	Gln	Thr
Ser	Pro 530	Ser	Ile	Leu	Val	Pro	Pro	Leu	Leu	Asp	Ala	Met	Asn	Lys	Asn

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn

545	550	555	560
Val Ser Met Lys Thr 565	Met Tyr Ala Pro Ala 570	Trp Leu Ser Met Gly 579	
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Gly Arg Arg Ile Lys 595	Ile		
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